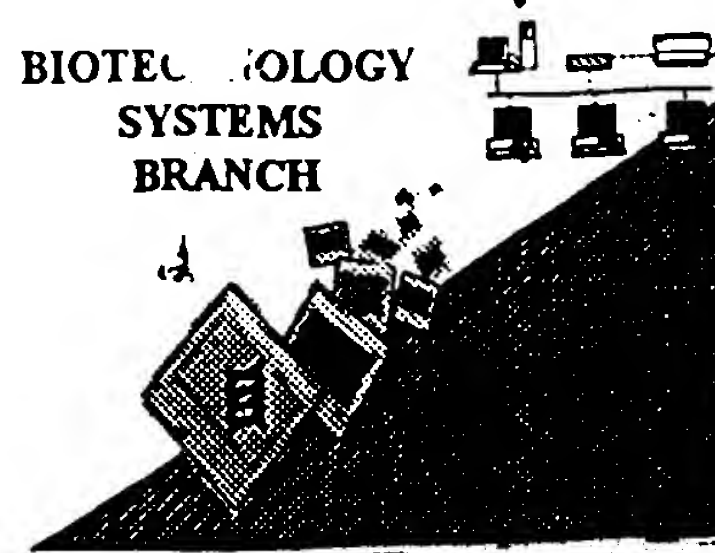


054
11/08

RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/982,262

Source: OIP

Date Processed by STIC: 11/2/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/982,262

DATE: 11/02/2001

TIME: 15:40:11

Input Set : A:\isph0612seq.txt

Output Set: N:\CRF3\11022001\I982262.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: C. Frank Bennett
 5 Christopher K. Mirabelli
 7 <120> TITLE OF INVENTION: OLIGONUCLEOTIDE MODULATION OF CELL ADHESION
 9 <130> FILE REFERENCE: ISPH-0612
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/982,262
 C--> 11 <141> CURRENT FILING DATE: 2001-10-18
 11 <150> PRIOR APPLICATION NUMBER: 09/659,288
 12 <151> PRIOR FILING DATE: 2000-09-12
 14 <150> PRIOR APPLICATION NUMBER: 09/128,496
 15 <151> PRIOR FILING DATE: 1998-08-03
 17 <150> PRIOR APPLICATION NUMBER: 08/440,740
 18 <151> PRIOR FILING DATE: 1995-05-12
 20 <150> PRIOR APPLICATION NUMBER: 08/063,167
 21 <151> PRIOR FILING DATE: 1993-05-17
 23 <150> PRIOR APPLICATION NUMBER: 07/969,151
 24 <151> PRIOR FILING DATE: 1993-02-10
 26 <150> PRIOR APPLICATION NUMBER: 08/007,997
 27 <151> PRIOR FILING DATE: 1993-01-21
 29 <160> NUMBER OF SEQ ID NOS: 86

Please see P. 3
 for explanations.

ERRORED SEQUENCES

372 <210> SEQ ID NO: 32
 373 <211> LENGTH: 20
 374 <212> TYPE: DNA
 375 <213> ORGANISM: Artificial Sequence
 377 <220> FEATURE:
 378 <223> OTHER INFORMATION: Antisense Oligonucleotide
 380 <400> SEQUENCE: 32
 E--> 381 acctctgctg ttctgatcc 20
 416 <210> SEQ ID NO: 36
 417 <211> LENGTH: 1
 418 <212> TYPE: DNA
 419 <213> ORGANISM: Artificial Sequence
 421 <220> FEATURE:
 422 <223> OTHER INFORMATION: Antisense Oligonucleotide
 424 <400> SEQUENCE: 36
 E--> 425 tgaagcaatc atgacttcaa g 21
 427 <210> SEQ ID NO: 37
 428 <211> LENGTH: 21
 429 <212> TYPE: DNA
 430 <213> ORGANISM: Artificial Sequence
 432 <220> FEATURE:
 433 <223> OTHER INFORMATION: Antisense Oligonucleotide
 435 <400> SEQUENCE: 37
 E--> 436 tataggagtt ttgatgtgaa 21

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/982,262

DATE: 11/02/2001

TIME: 15:40:11

Input Set : A:\isph0612seq.txt

Output Set: N:\CRF3\11022001\I982262.raw

482 <210> SEQ ID NO: 42

483 <211> LENGTH: 21

484 <212> TYPE: DNA

485 <213> ORGANISM: Artificial Sequence

487 <220> FEATURE:

488 <223> OTHER INFORMATION: Antisense Oligonucleotide

490 <400> SEQUENCE: 42

E--> 491 cctgaagcca gtgaggcccg 21

834 <210> SEQ ID NO: 74

835 <211> LENGTH: 20

836 <212> TYPE: DNA

837 <213> ORGANISM: Artificial Sequence

839 <220> FEATURE:

840 <223> OTHER INFORMATION: Antisense Oligonucleotide

842 <400> SEQUENCE: 74

E--> 843 tgattctttt gaacttaaaa gga 20

856 <210> SEQ ID NO: 76

857 <211> LENGTH: 190

858 <212> TYPE: DNA

859 <213> ORGANISM: Artificial Sequence

861 <220> FEATURE:

862 <223> OTHER INFORMATION: Antisense Oligonucleotide

864 <400> SEQUENCE: 76

E--> 865 cataagcaca ttattgtc 19

966 <210> SEQ ID NO: 86

967 <211> LENGTH: 20

968 <212> TYPE: DNA

969 <213> ORGANISM: Artificial Sequence

971 <220> FEATURE:

972 <223> OTHER INFORMATION: Antisense Oligonucleotide

974 <400> SEQUENCE: 86

975 agggccactg ctcgtccaca 20

E--> 978 16 delete

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/982,262

DATE: 11/02/2001

TIME: 15:40:12

Input Set : A:\isph0612seq.txt

Output Set: N:\CRF3\11022001\I982262.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:381 M:254 E: No. of Bases conflict, LENGTH:Input:20 Counted:19 SEQ:32
L:381 M:252 E: No. of Seq. differs, <211>LENGTH:Input:20 Found:19 SEQ:32
L:425 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1 Found:21 SEQ:36
L:436 M:254 E: No. of Bases conflict, LENGTH:Input:21 Counted:20 SEQ:37
L:436 M:252 E: No. of Seq. differs, <211>LENGTH:Input:21 Found:20 SEQ:37
L:491 M:254 E: No. of Bases conflict, LENGTH:Input:21 Counted:20 SEQ:42
L:491 M:252 E: No. of Seq. differs, <211>LENGTH:Input:21 Found:20 SEQ:42
L:843 M:254 E: No. of Bases conflict, LENGTH:Input:20 Counted:23 SEQ:74
L:843 M:252 E: No. of Seq. differs, <211>LENGTH:Input:20 Found:23 SEQ:74
L:865 M:252 E: No. of Seq. differs, <211>LENGTH:Input:190 Found:19 SEQ:76
L:978 M:254 E: No. of Bases conflict, LENGTH:Input:16 Counted:20 SEQ:86